

E. Lazar-West

# 11  
9/23/02

RAW SEQUENCE LISTING DATE: 09/23/2002  
 PATENT APPLICATION: US/09/639,273 TIME: 12:47:34

Input Set : N:\Crf3\RULE60\09639273.raw  
 Output Set: N:\CRF4\09232002\I639273.raw

-----SEQUENCE LISTING-----

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Innes, Michael  
 6 Creasey, Abla

8 (ii) TITLE OF INVENTION: Production of Tissue Factor Pathway  
 9 Inhibitor

11 (iii) NUMBER OF SEQUENCES: 7

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Chiron Corporation

15 (B) STREET: 4560 Horton St.

16 (C) CITY: Emeryville

17 (D) STATE: CA

18 (E) COUNTRY: USA

19 (F) ZIP: 94608

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30B

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/639,273

C--> 29 (B) FILING DATE: 15-Aug-2000

30 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/08/286,530

35 (B) FILING DATE: 05-AUG-1994

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Savereide, Paul B.

39 (B) REGISTRATION NUMBER: 36,914

40 (C) REFERENCE/DOCKET NUMBER: 0991.001

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 510-601-2585

44 (B) TELEFAX: 510-655-3542

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1065 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: double

53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: other nucleic acid

57 (iii) HYPOTHETICAL: NO

59 (iv) ANTI-SENSE: NO

62 (ix) FEATURE:

ENTERED

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63	(A) NAME/KEY: CDS	
64	(B) LOCATION: 1..1056	
67	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
69	ATG CAG ATC TTC GTC AAG ACT TTG ACC GGT AAA ACC ATA ACA TTG GAA	48
70	Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu	
71	1 5 10 15	
73	GTT GAA TCT TCC GAT ACC ATC GAC AAC GTT AAG TCG AAA ATT CAA GAC	96
74	Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp	
75	20 25 30	
77	AAG GAA GGT ATC CCT CCA GAT CAA CAA AGA TTG ATC TTT GCC GGT AAG	144
78	Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys	
79	35 40 45	
81	CAG CTA GAA GAC GGT AGA ACG CTG TCT GAT TAC AAC ATT CAG AAG GAG	192
82	Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu	
83	50 55 60	
85	TCC ACC TTA CAT CTT GTG CTA AGG CTC CGC GGT GGT GAT TCT GAG GAA	240
86	Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Asp Ser Glu Glu	
87	65 70 75 80	
89	GAT GAA GAA CAC ACA ATT ATC ACA GAT ACG GAG TTG CCA CCA CTG AAA	288
90	Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys	
91	85 90 95	
93	CTT ATG CAT TCA TTT TGT GCA TTC AAG GCG GAT GAT GGC CCA TGT AAA	336
94	Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys	
95	100 105 110	
97	GCA ATC ATG AAA AGA TTT TTC TTC AAT ATT TTC ACT CGA CAG TGC GAA	384
98	Ala Ile Met Lys Arg Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu	
99	115 120 125	
101	GAA TTT ATA TAT GGG GGA TGT GAA GGA AAT CAG AAT CGA TTT GAA AGT	432
102	Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser	
103	130 135 140	
105	CTG GAA GAG TGC AAA AAA ATG TGT ACA AGA GAT AAT GCA AAC AGG ATT	480
106	Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile	
107	145 150 155 160	
109	ATA AAG ACA ACA TTG CAA CAA GAA AAG CCA GAT TTC TGC TTT TTG GAA	528
110	Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu	
111	165 170 175	
113	GAA GAT CCT GGA ATA TGT CGA GGT TAT ATT ACC AGG TAT TTT TAT AAC	576
114	Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn	
115	180 185 190	
117	AAT CAG ACA AAA CAG TGT GAA CGT TTC AAG TAT GGT GGA TGC CTG GGC	624
118	Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly	
119	195 200 205	
121	AAT ATG AAC AAT TTT GAG ACA CTG GAA GAA TGC AAG AAC ATT TGT GAA	672
122	Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu	
123	210 215 220	
125	GAT GGT CCG AAT GGT TTC CAG GTG GAT AAT TAT GGA ACC CAG CTC AAT	720
126	Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn	
127	225 230 235 240	
129	GCT GTG AAT AAC TCC CTG ACT CCG CAA TCA ACC AAG GTT CCC AGC CTT	768

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130	Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu			
131	245	250	255	
133	TTT GAA TTT CAC GGT CCC TCA TGG TGT CTC ACT CCA GCA GAC AGA GGA	816		
134	Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly			
135	260	265	270	
137	TTG TGT CGT GCC AAT GAG AAC AGA TTC TAC TAC AAT TCA GTC ATT GGG	864		
138	Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly			
139	275	280	285	
141	AAA TGC CGC CCA TTT AAG TAC AGT GGA TGT GGG GGA AAT GAA AAC AAT	912		
142	Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Asn Glu Asn Asn			
143	290	295	300	
145	TTT ACT TCC AAA CAA GAA TGT CTG AGG GCA TGT AAA AAA GGT TTC ATC	960		
146	Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile			
147	305	310	315	320
149	CAA AGA ATA TCA AAA GGA GGC CTA ATT AAA ACC AAA AGA AAA AGA AAG	1008		
150	Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys			
151	325	330	335	
153	AAG CAG AGA GTG AAA ATA GCA TAT GAA GAA ATT TTT GTT AAA AAT ATG	1056		
154	Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met			
155	340	345	350	
157	TGAGTCGAC	1065		
160	(2) INFORMATION FOR SEQ ID NO: 2:			
162	(i) SEQUENCE CHARACTERISTICS:			
163	(A) LENGTH: 352 amino acids			
164	(B) TYPE: amino acid			
165	(D) TOPOLOGY: linear			
167	(ii) MOLECULE TYPE: protein			
169	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
171	Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu			
172	1	5	10	15
174	Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp			
175	20	25	30	
177	Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys			
178	35	40	45	
180	Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu			
181	50	55	60	
183	Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Asp Ser Glu Glu			
184	65	70	75	80
186	Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys			
187	85	90	95	
189	Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys			
190	100	105	110	
192	Ala Ile Met Lys Arg Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu			
193	115	120	125	
195	Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser			
196	130	135	140	
198	Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile			
199	145	150	155	160
201	Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu			

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202	165	170	175
204	Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn		
205	180	185	190
207	Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly		
208	195	200	205
210	Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu		
211	210	215	220
213	Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn		
214	225	230	235
216	Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu		
217	245	250	255
219	Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly		
220	260	265	270
222	Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly		
223	275	280	285
225	Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn		
226	290	295	300
228	Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile		
229	305	310	315
231	Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys		
232	325	330	335
234	Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met		
235	340	345	350

238 (2) INFORMATION FOR SEQ ID NO: 3:

240 (i) SEQUENCE CHARACTERISTICS:  
241 (A) LENGTH: 276 amino acids  
242 (B) TYPE: amino acid  
243 (C) STRANDEDNESS: single  
244 (D) TOPOLOGY: linear

246 (ii) MOLECULE TYPE: peptide

251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

253	Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu		
254	1	5	10
256	Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp		
257	20	25	30
259	Gly Pro Cys Arg Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr		
260	35	40	45
262	Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn		
263	50	55	60
265	Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn		
266	65	70	75
268	Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe		
269	85	90	95
271	Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg		
272	100	105	110
274	Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly		
275	115	120	125
277	Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys		
278	130	135	140

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280 Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly  
281 145 150 155 160  
283 Thr Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys  
284 165 170 175  
286 Val Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro  
287 180 185 190  
289 Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn  
290 195 200 205  
292 Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly  
293 210 215 220  
295 Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys  
296 225 230 235 240  
298 Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys  
299 245 250 255  
301 Arg Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe  
302 260 265 270  
304 Val Lys Asn Met  
305 275

307 (2) INFORMATION FOR SEQ ID NO: 4:

309 (i) SEQUENCE CHARACTERISTICS:

310 (A) LENGTH: 9 base pairs  
311 (B) TYPE: nucleic acid  
312 (C) STRANDEDNESS: single  
313 (D) TOPOLOGY: linear

315 (ii) MOLECULE TYPE: other nucleic acid

316 (A) DESCRIPTION: /desc = "primer"

321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

323 CCGCGGGGC

9

325 (2) INFORMATION FOR SEQ ID NO: 5:

327 (i) SEQUENCE CHARACTERISTICS:

328 (A) LENGTH: 23 base pairs  
329 (B) TYPE: nucleic acid  
330 (C) STRANDEDNESS: single  
331 (D) TOPOLOGY: linear

333 (ii) MOLECULE TYPE: other nucleic acid

334 (A) DESCRIPTION: /desc = "primer"

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

341 GCTCCGCGGT GGCGATTCTG AGG

23

343 (2) INFORMATION FOR SEQ ID NO: 6:

345 (i) SEQUENCE CHARACTERISTICS:

346 (A) LENGTH: 24 base pairs  
347 (B) TYPE: nucleic acid  
348 (C) STRANDEDNESS: single  
349 (D) TOPOLOGY: linear

351 (ii) MOLECULE TYPE: other nucleic acid

352 (A) DESCRIPTION: /desc = "primer"

357 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

359 TCTGTCGACT CACATATTAAAC

24

361 (2) INFORMATION FOR SEQ ID NO: 7:

RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 09/23/2002  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 160  
Seq#:2; Line(s) 238  
Seq#:3; Line(s) 307  
Seq#:4; Line(s) 325  
Seq#:5; Line(s) 343  
Seq#:6; Line(s) 361

**VERIFICATION SUMMARY****PATENT APPLICATION:** US/09/639,273**DATE:** 09/23/2002**TIME:** 12:47:35**Input Set :** N:\Crf3\RULE60\09639273.raw  
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]